

```

QY 1845 TTTGGCCATTGTATGATGATGTTGGTGTGTTTAAACATGGTATGAAATGTTGTTACTT 1904
Db 1861 TTTGGCCATTGTATGATGATGTTGGTGTGTTTAAACATGGTATGAAATGTTGTTACTT 1920
QY 1905 CTGTCAGAGAAACAGAGTACTAATCTCCAAATTAATAAATTTTAAACATGTAAATA 1964
Db 1921 CTGTCAGAGAAACAGAGTACTAATCTCCAAATTAATAAATTTTAAACATGTAAATA 1980
QY 1965 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1994
Db 1981 TTTGCTTTTGAACAACAAGATTACAGAA 2010

RESULT 4
HUM3H3M
LOCUS
DEFINITION Homo sapiens 3-hydroxy-3-methylglutaryl coenzyme A synthase mRNA,
complete cds.
ACCESSION L25798
VERSION L25798.1 GI:410027
KEYWORDS 3-hydroxy-3-methylglutaryl coenzyme A synthase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1650)
Rokosz, L.B., Boulton, D.A., Butkiewicz, E.A., Sanyal, G., Cueto, M.A.,
Lachance, P.A. and Hermes, J.D.
HUMAN CYTOPLASMIC 3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE:
expression, purification, and characterization of recombinant
wild-type and Cys129 mutant enzymes
Arch. Biochem. Biophys. 312 (1), 1-13 (1994)
94304197
7913309
COMMENT Original source text: Homo sapiens fetal adrenal cdna to mRNA.
FEATURES
Location/Qualifiers
1..1650
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="fetal adrenal"
22..1584
/codon_start=1
/product="3-hydroxy-3-methylglutaryl coenzyme A synthase"
/protein_id="AA062411.1"
/db_xref="GI:410028"
/translation="MPSGLPINAECWPKDVGIVALEIYPPSYVDQBLEKVDGVDA
GKTHIGQAKQFCDREINSCMTVQNLNERNLSYDCIGRLEVGTETLIDKSK
SVKTNLMQLFEESGNTDIEGIDTNACYGGTAAVFNAVNWIESSWDGRYALVAGDI
AVATGNARTGGVAVALLIGPNAPLIFERGLRTHMQHAYDFYKPMLSYPIVDG
KLSTQCYLSALDRCYVYCKIHAQWQKGNKDFINDPFMIHPSYCKLVQKSLA
RMLNDPLNDONRDKNSIYSGLEAFGDKLEDYDFDRVEKATMKASSSELFSQKTLA
LLVSNONGMYTSSVYGLASVLAQYSPQOLACKRIGVESYSGSLAATLYSLKVTDQ
TPGSALDKITASLCLDKSLRDSRTGVAPDVPFAENMKLRDTHLVNYIIFQGSIDSLFE
GTWLVLRDEKHKRTYARRTPNDTDLDEGVGLVHNSIATEHIPSPAKKVPRLPATAA
EPEAAVISNGEH"
CDS
source
Query Match 68.4%; Score 1370; DB 9; Length 1650;
Best Local Similarity 92.0%; Pred. No. 1e-287;
Matches 1509; Conservative 0; Mismatches 5; Indels 126; Gaps 1;
QY 134 GCTTTTCAACATGCCCTGGATCACTTCCTTGAATGAGAAGCTTGTCGCCAAAAGATG 193
Db 11 GCTCTTTCAACATGCCCTGGATCACTTCCTTGAATGAGAAGCTTGTCGCCAAAAGATG 70
QY 194 TGGGAATGTGTCCTTGAGATCTATTTCTTCTCAATATGTTGATCAAGCAGATTGG 253
Db. 71 TTGGGATGTGTCCTTGAGATCTATTTCTTCTCAATATGTTGATCAAGCAGATTGG 130
QY 254 AAAAAATATGATGGTGTAGATGCTGGAAGTATACCATTTGGCTGGGCCAGGCCAAGATGG 313
131 AAAAAATATGATGGTGTAGATGCTGGAAGTATACCATTTGGCTGGGCCAGGCCAAGATGG 190

```

```

QY 314 GCTTCTGCACAGATAGAGAAGATTAATTAATCTCTTTGCACTGTGTTTCAAGATCTTA 373
Db 191 GCTTCTGCACAGATAGAGAAGATTAATTAATCTCTTTGCACTGTGTTTCAAGATCTTA 250
QY 374 TGGAGAGAAATAAACCCTTTCCTATGATTCGATTCGGCGGCTGGAAGTTGGAAACAGAGCAA 433
Db 251 TGGAGAGAAATAAACCCTTTCCTATGATTCGATTCGGCGGCTGGAAGTTGGAAACAGAGCAA 310
QY 434 TCATCGACAAATCAAAAGTCTGTGAAGACTAATTTGATGCAGCTGTTTGAAGAGTCTGGGA 493
Db 311 TCATCGACAAATCAAAAGTCTGTGAAGACTAATTTGATGCAGCTGTTTGAAGAGTCTGGGA 370
QY 494 ATACAGATATAGAAAGGAATCGACACAACTAATGCTATGCTATGAGGGCACAGCTGCTGCT 553
Db 371 ATACAGATATAGAAAGGAATCGACACAACTAATGCTATGCTATGAGGGCACAGCTGCTGCT 430
QY 554 TCAATGCTGTAACTCGGATTCAGTCCAGCTCTTGGAT----- 591
Db 431 TCAATGCTGTAACTCGGATTCAGTCCAGCTCTTGGATGGACGGTATGCCCTGGTAGTTG 490
QY 592 ----- 591
Db 491 CAGGAGATATTGCTGTATATGCCACAGGAATGCTAGACCTACAGGTGGAGTTGGAGCAG 550
QY 592 -----GGGCTTCGTGGGACAC 607
Db 551 TAGCTCTGCTAATTGGGCCAAATGCTCCTTTAATTTTGAACGAGGGCTTCGTGGGACAC 610
QY 608 ATATCAACATGCTCTATGATTTTACAAAGCCTGATGCTATCTCTGAATATCTCTATAGTAG 667
Db 611 ATATGCAACATGCTCTATGATTTTACAAAGCCTGATGCTATCTCTGAATATCTCTATAGTAG 670
QY 668 ATGGAATACTCTCCATACAGTGTCTACCTCAGTCGATTAGACCGCTGCTACTCTCTACT 727
Db 671 ATGGGAAATCTCTCCATACAGTGTCTACCTCAGTCGATTAGACCGCTGCTACTCTACT 730
QY 728 GCAAAAGATCCATGCCCGCAGTGGCAGAAAGAGGAAATGATAAAGATTTTACCTTGAATG 787
Db 731 GCAAAAGATCCATGCCCGCAGTGGCAGAAAGAGGAAATGATAAAGATTTTACCTTGAATG 790
QY 788 ATTTTGGCTTCATGATCTTTCACTCACCATATTTGAAACTGGTTTCAAGAAATCTCTAGCTC 847
Db 791 ATTTTGGCTTCATGATCTTTCACTCACCATATTTGAAACTGGTTTCAAGAAATCTCTAGCTC 850
QY 848 GGATGTTGCTGAATGACTTCCTTAATGACCAAGATAGAGATAAATAATAGTATCTATAGTG 907
Db 851 GGATGTTGCTGAATGACTTCCTTAATGACCAAGATAGAGATAAATAATAGTATCTATAGTG 910
QY 908 GCTTGAAGCCCTTTGGGGATGTTTAAATTTAGAAGACACCTACTTTTGAAGATGTGGAGA 967
Db 911 GCTTGAAGCCCTTTGGGGATGTTTAAATTTAGAAGACACCTACTTTTGAAGATGTGGAGA 970
QY 968 AGGCATTTATGAAGCTAGCTCTGAACTCTTCACTGAGAAACAAAGGCATCTTTACTTTG 1027
Db 971 AGGCATTTATGAAGCTAGCTCTGAACTCTTCACTGAGAAACAAAGGCATCTTTACTTTG 1030
QY 1028 TATCAAAATCAAAATGGAATATGTACACATCTTCAAGTATATGGTTTCCCTTCGATCTGTC 1087
Db 1031 TATCAAAATCAAAATGGAATATGTACACATCTTCAAGTATATGGTTTCCCTTCGATCTGTC 1090
QY 1088 TAGCAGATCTACCTCAGCAATTTAGCAGGAGAGAAATTTGGAGTGTGTTTCTTATGTTT 1147
Db 1091 TAGCAGATCTACCTCAGCAATTTAGCAGGAGAGAAATTTGGAGTGTGTTTCTTATGTTT 1150
QY 1148 CTGGTTTGGCTGCCACTCTGTACTCTCTTAAAGTCACACAGATGCTACACGGGGCTG 1207
Db 1151 CTGGTTTGGCTGCCACTCTGTACTCTCTTAAAGTCACACAGATGCTACACGGGGCTG 1210
QY 1208 CTCTTGATAAATAACACAGCAAGTTTATGTGATCTTAAATCAAGGCTTGATTCAGAACTG 1267
Db 1211 CTCTTGATAAATAACACAGCAAGTTTATGTGATCTTAAATCAAGGCTTGATTCAGAACTG 1270

```

QY	1268	GTGTGGCACCAGATGTCTTCGCTGAAAAATGAGAGCTCAGAGAGCACCCATCATTTGG	1327
Db	1271	GTGTGGCACCAGATGTCTTCGCTGAAAAATGAGAGCTCAGAGAGCACCCATCATTTGG	1330
QY	1328	TCAACTATATTCCCCAGGGTTCAATAGATTCACTCTTTGAAGGAACGTGGTACTTAGTTA	1387
Db	1331	TCAACTATATTCCCCAGGGTTCAATAGATTCACTCTTTGAAGGAACGTGGTACTTAGTTA	1390
QY	1388	GGTGTGATGAAGACACAGAAACCTTAGCTCGGGGTCCCACTCCCAATGATGACACTT	1447
Db	1391	GGTGTGATGAAGACACAGAAACCTTAGCTCGGGGTCCCACTCCCAATGATGACACTT	1450
QY	1448	TGGATGAAGGAGTAGGACTTGTGCATTCAAAATAGCAACTGAGCATATTCGAAGCCCTG	1507
Db	1451	TGGATGAAGGAGTAGGACTTGTGCATTCAAAATAGCAACTGAGCATATTCGAAGCCCTG	1510
QY	1508	CCAGAAAGTACCAAGACTCCCTGCCACAGCAGCAGACCTGAGCAGCTGTGCTATTAGTA	1567
Db	1511	CCAGAAAGTACCAAGACTCCCTGCCACAGCAGCAGACCTGAGCAGCTGTGCTATTAGTA	1570
QY	1568	ATGGGGAACATTTAGATATCTCTGTGAGGTGCAAGACTTCAGGGTGGGGTGGGCATGGGGT	1627
Db	1571	ATGGGGAACATTTAGATATCTCTGTGAGGTGCAAGACTTCAGGGTGGGGTGGGCATGGGGT	1630
QY	1628	GGGGGTATGGGAACAGTTGG	1647
Db	1631	GGGGGTATGGGAACAGTTGG	1650
RESULT 5			
LOCUS	BT007302	1563 bp mRNA linear PRI 13-MAY-2003	
DEFINITION	Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble) mRNA, complete cds.		
ACCESSION	BT007302.1	GI:30583442	
VERSION	FLI CDNA.		
KEYWORDS	Source		
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1563)		
TITLE	Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.		
JOURNAL	Cloning of human full-length cDNAs in BD Creator(TM) System Donor vector		
REFERENCE	2 (bases 1 to 1563)		
AUTHORS	Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA		
COMMENT	This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD in-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.		
FEATURES			
source	Location/Qualifiers		
	1..1563		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="GH00878X1.0"		
	/clone_lib="BD Creator(TM) CDS Library derived from MGC collection"		

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2004, 12:56:26 / Search time 44 Seconds
(without alignments)
565.671 Million cell updates/sec

Title: US-10-622-516-2

Perfect score: 2511

Sequence: 1 MPGLPLNAEACWPKDVGIV.....PRLPATRAEPEAAVISNGEH 478

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2480	98.8	520	1	HMCS HUMAN
2	2362	94.1	520	1	HMCS RAT
3	2352	93.7	520	1	HMCS CRIGR
4	2097	83.5	522	1	HMCS CHICK
5	1513	60.3	508	1	HMCM HUMAN
6	1494	59.5	508	1	HMCM RAT
7	1493	59.5	480	1	HMCM MOUSE
8	1466	58.4	508	1	HMCM PIG
9	1352.5	53.9	453	1	HMCI BLAGE
10	1272.5	50.7	455	1	HMCI BLAGE
11	980	39.0	461	1	HMCS ARATH
12	950.5	37.9	491	1	HMCS YEAST
13	900	35.8	447	1	HMCS SCHPO
14	705	28.1	462	1	HMCS CAEEL
15	249	9.9	163	1	HMCS DICDI
16	152	6.1	350	1	YD79 METKA
17	147	5.3	345	1	PKSG BRCSU
18	145.5	5.8	346	1	Y792 METTH
19	144	5.7	350	1	Y677 PYRHO
20	138.5	5.5	350	1	Y972 PYRHO
21	135	5.4	349	1	Y871 METMA
22	132.5	5.3	343	1	Y015 ARCFU
23	130	5.2	350	1	Y185 PYRAE
24	127	5.1	349	1	Y4E1 METAC
25	126.5	5.0	350	1	YD69 PYRAB
26	123.5	4.9	716	1	BGAL THEVO
27	123	4.9	351	1	Y132 THEVO
28	122	4.9	345	1	YF46 METJA
29	122	4.9	351	1	Y5E5 THEAC
30	121	4.8	580	1	N056 MOUSE
31	118.5	4.7	596	1	N056 HUMAN
32	116	4.6	348	1	YD49 SULTO
33	107.5	4.3	776	1	TOP1 RICPR

ALIGNMENTS

RESULT 1

ID	HMCS HUMAN	STANDARD;	PRT;	520 AA.
AC	Q01581;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Hydroxymethylglutaryl-CoA synthase, cytoplasmic (EC 2.3.3.10) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase).			
GN	HMGCS1 OR HMGCS.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fibroblast;			
RX	MEDLINE=93041939; PubMed=1358203;			
RA	Russ A.P., Ruzicka V., Maerz W., Appelhaus H., Gross W.;			
RT	"Amplification and direct sequencing of a cDNA encoding human cytosolic 3-hydroxy-3-methylglutaryl-coenzyme A synthase."			
RL	Biochim. Biophys. Acta 1132:329-331(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS.			
RC	TISSUE=Fetal adrenal gland;			
RX	MEDLINE=94304197; PubMed=7913309;			
RA	Rokosz L.L., Boulton D.A., Butkiewicz E.A., Sanyal G., Cueto M.A.,			
RA	Lachance P.A., Hermes J.D.;			
RT	"Human cytoplasmic 3-hydroxy-3-methylglutaryl coenzyme A synthase: expression, purification, and characterization of recombinant wild-type and Cys129 mutant enzymes."			
RL	Arch. Biochem. Biophys. 312:1-13(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madsen A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madsen A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

P09831 escherichia
Q09291 caenorhabdi
P05201 mus musculu
Q62859 mus musculu
Q10011 caenorhabdi
Q01529 podospora a
Q02135 lactococcus
Q9x597 bacillus th
Q921h1 rickettsia
P05519 bacillus th
Q87tn4 vibrio para

34 106.5 4.2 1517 1 GLTB ECOLI
35 106 4.2 367 1 Y0L2 CAEEL
36 105 4.2 412 1 AATC_MOUSE
37 105 4.2 3358 1 PGCV_MOUSE
38 103 4.1 489 1 YSV5 CAEEL
39 103 4.1 1197 1 DPOW_PODAN
40 102 4.1 360 1 H1S8 LACLA
41 102 4.1 1163 1 CQAA BACTF
42 101 4.0 365 1 Y173 ARPE
43 100.5 4.0 776 1 TOPI_RICCN
44 100 4.0 1136 1 C4BA_BACTI
45 99.5 4.0 494 1 ILVC_VIBPA

-!- FUNCTION: This enzyme condenses acetyl-CoA with acetoacetyl-CoA to form HMG-CoA, which is the substrate for HMG-CoA reductase.
 -!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + acetoacetyl-CoA = (S)-3-hydroxy-3-methylglutaryl-CoA + CoA.
 -!- PATHWAY: PRODUCTION OF MEVALONATE FROM HMG-CoA PRIOR TO THE SYNTHESIS OF STEROLS SUCH AS CHOLESTEROL AND ISOPRENOLIDS.
 -!- SUBCELLULAR LOCATION: Cytoplasmic.
 -!- SIMILARITY: Belongs to the HMG-CoA synthase family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; X66435; CAA47061.1; -.
EMBL; L25798; AAA62411.1; -.
EMBL; BC000297; AAH00297.1; -.
PIR; S27197; S27197.
PIR; S45497; S45497.
Genew; HGNC:5007; HMGCS1.
MIM; 142340; -.
GO; GO:0005737; Cytosolasm; TAS.
GO; GO:0005825; C-soluble fraction; TAS.
GO; GO:0004421; F-hydroxymethylglutaryl-CoA synthase activity; TAS.
InterPro; IPR000590; HMG CoA synt AS.
InterPro; IPR008260; HMG CoA synth.
Pfam; PF01154; HMG CoA synt; 1.
PROSITE; PS01226; HMG CoA SYNTHASE; 1.
Transferase; Cholesterol biosynthesis; Multigene family.
ACT SITE 129 139
MUTAGEN 129 139
CONFLICT 248
CONFLICT 251
CONFLICT 239
C->A, S; LOSS OF ACTIVITY.
G -> A (IN REF. 1).
K -> N (IN REF. 1).
E -> K (IN REF. 1).

```

          98.8%; Score 2480; DB 1; Length 520;
          at Local Similarity 91.9%;
          ches 478; Conservative 0; Mismatches 7; Indels 42; Gaps 1;

1  MPGSPLPNAEACWPKDVGIVALEIYFYSQYVDQAELEKYGVDGAGKYTIGLGQAKMGFCT 60
1  MPGSPLPNAEACWPKDVGIVALEIYFYSQYVDQAELEKYGVDGAGKYTIGLGQAKMGFCT 60
61  DREDINSLCMTVYQNLMEERNLSDYDCIGRLEVGTETIIDKSKSVKTNLMQLFEESGNTDI 120
61  DREDINSLCMTVYQNLMEERNLSDYDCIGRLEVGTETIIDKSKSVKTNLMQLFEESGNTDI 120
121  EGIDTTNACYGGTAAVFNAVNWIESSWD----- 149
121  EGIDTTNACYGGTAAVFNAVNWIESSWDGGRYALVWAGDIATVATGNAPTGGGAVALL 180
150  -----GLRGTHMGHAYDFPKDMLSEYPIVDGKLISIQCYLSALDRCYSYVCKKI 198
181  IGPNAPLIFERGLRGTHMGHAYDFPKDMLSEYPIVDGKLISIQCYLSALDRCYSYVCKKI 240
199  HAQWQKEGNDKQFTLNDPFGMI FHSFPYCKLVQKSLARPMILNDQNDRDKNISYSGLEA 258
241  HAQWQKEGNDKQFTLNDPFGMI FHSFPYCKLVQKSLAERMLNDQNDRDKNISYSGLEA 300
259  FGDVKLEEDTYFDRDVEKAPMKASSBSPQKTKASLLVSNQNGNMYTSSVYGSLASVLAQY 318
301  FGDVKLEEDTYFDRDVEKAPMKASSBSPQKTKASLLVSNQNGNMYTSSVYGSLASVLAQY 360
319  SPOQLAGKRIGVFSGGSLAATLYSLKVTQDATPGSALDKITASLCDLKSRLDSTGVAP 378
361  SPOQLAGKRIGVFSGGSLAATLYSLKVTQDATPGSALDKITASLCDLKSRLDSTGVAP 420

```

QY	379	DVFAENKLEEDTHLVNVI	PGSDSDLSIEGTHVLRVDEKHRTYAARRPTNDTDLDEG	439				
DB	421	DVFAENKLEEDTHLVNVI	PGSDSDLSIEGTHVLRVDEKHRTYAARRPTNDTDLDEG	480				
QY	439	VGLVHSNIAETHPISPAKKVPRLPATAAPEEAAVISINGEH	478					
DB	481	VGLVHSNIAETHPISPAKKVPRLPATAAPEEAAVISINGEH	520					
RESULT 2								
HMCS RAT								
ID	HMCS	RAT	STANDARD;	PRT; 520 AA.				
AC	P17425;							
DT	01-AUG-1990	(Rel. 15, Created)						
DT	01-AUG-1990	(Rel. 15, Last sequence update)						
DT	10-OCT-2003	(Rel. 42, Last annotation update)						
DE	Hydroxymethylglutaryl-CoA synthase, cytoplasmic (EC 2.3.3.10) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase).							
DE	HMGCS1 OR HMCS.							
GN	Rattus norvegicus (Rat).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.							
OX	NCBI_TaxID=10116;							
RP	[1]							
RP	SEQUENCE FROM N.A.							
ST	STRAINS=Sprague-Dawley; TISSUE=Liver;							
RC	MEDLINE=90301491; PubMed=1972979;							
RA	Ayte J., Gil-Gomez G., Hegardt P.G.;							
RT	Nucleotide sequence of a rat liver cDNA encoding the cytosolic 3-hydroxy-3-methylglutaryl coenzyme A synthase.";							
RL	Nucleic Acids Res. 18:3642-3642(1990).							
CC	FUNCTION: This enzyme condenses acetyl-CoA with acetoacetyl-CoA to form HMG-CoA, which is the substrate for HMG-CoA reductase.							
CC	CATALYTIC ACTIVITY: Acetyl-CoA + H2O + acetoacetyl-CoA -> (S)-3-hydroxy-3-methylglutaryl-CoA + CoA.							
CC	PATHWAY: PRODUCTION OF MEVALONATE FROM HMG-CoA PRIOR TO THE SYNTHESIS OF STEROLS SUCH AS CHOLESTEROL AND ISOPRENOIDS.							
CC	SUBCELLULAR LOCATION: Cytoplasmic.							
CC	SIMILARITY: Belongs to the HMG-CoA synthase family.							
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch).							
CC	EMBL; X52625; CAA36852.1; ..							
DR	PIR; S12736; S12736.							
DR	InterPro; IPR000590; HMG CoA synt AS.							
DR	InterPro; IPR008260; HMG CoA synth.							
DR	Pfam; PF01154; HMG CoA synt; 1.							
DR	PROSITE; PS01226; HMG CoA SYNTHASE; 1.							
KN	Transferase; Cholesterol Biosynthesis; Multigene family.							
FT	ACT_SITE 129 129 POTENTIAL.							
SQ	SEQUENCE 520 AA; 57433 MW; CB213A27B0C177CB CRC64;							
Query Match								
Best Local Similarity 94.1%; Score 2362; DB 1; Length 520;								
Matches 455; Conservative 11; Mismatches 12; Indels 42; Gaps 1;								
QY	1	MPGSLPNAEACPKDVGIVALEIYFPQSQVDALEKYGVDGAKYTGIGLQAKMGFCT	60					
DB	1	MPGSLPNAEACPKDVGIVALEIYFPQSQVDALEKYGVDGAKYTGIGLQAKMGFCT	60					
QY	61	DREDINSLCTVQKLMERNLSYDCIGRLVGTETIIDKSKSVKTNLMQLFEESGNTDI	120					
DB	61	DREDINSLCTVQKLMERNLSYDCIGRLVGTETIIDKSKSVKTNLMQLFEESGNTDI	120					
QY	121	EGIDTTNACYGGAATVFNANVNISSSSWD-----	149					

13